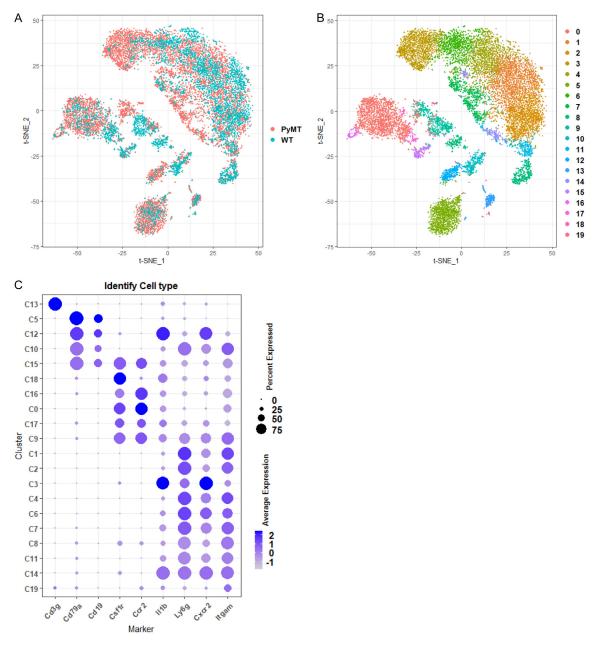


Supplementary Figure 1. Gene profiles of the two NanoString panels. A. The bar chart of the Pearson correlation coefficients between genes in the two NanoString panels. The means and standard deviations of correlations were estimated using all pairs of triplicates between panels and confirmed to have high consistency (correlation = 0.88-0.95). B. The scatter plot of PC1 and PC2 from the PCA of the two panels.



Supplementary Figure 2. Identification and annotation of clusters in the scRNA-seq data. In the t-SNE plot, the cells were colored based on the PyMT and WT mice or Seurat clusters. A. The cell distributions from the t-SNE plot. B. The clusters identified using integrated analysis in the R package Seurat. C. The dot plot of the average expression and percent expression of marker genes in each cluster.